



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
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- (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS:
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(E) COUNTRY: USA
(F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/903,068
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- (vii) PRIOR APPLICATION DATE:
(A) APPLICATION NUMBER: 08/436,265
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- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/GB93/02367
(B) FILING DATE: November 17, 1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9224057.1
(B) FILING DATE: November 17, 1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304677.9
(B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304680.3
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- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9311047.6
(B) FILING DATE: May 28, 1993

- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 9313763.6
 (B) FILING DATE: July 2, 1993
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 9316099.2
 (B) FILING DATE: August 3, 1993
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 321344.5
 (B) FILING DATE: October 15, 1993
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1984 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA	60
AGAAACATTT TTGCTCCAGC CCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC	120
GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT	180
CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GTCCGCCGA	240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC	294
Met Thr Leu Gly	
1	
TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG	342
Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln	
5 10 15 20	
GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT	390
Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys	
25 30 35	
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA	438
Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr	
40 45 50	
GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC	486
Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly	
55 60 65	

TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC	534
Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe	
70 75 80	
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC	582
Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser	
85 90 95 100	
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT	630
Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp	
105 110 115	
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG	678
Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu	
120 125 130	
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG	726
Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu	
135 140 145	
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG	774
Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu	
150 155 160	
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT	822
Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser	
165 170 175 180	
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG	870
Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg	
185 190 195	
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC	918
Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	
200 205 210	
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC	966
Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val	
215 220 225	
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG	1014
Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu	
230 235 240	
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC	1062
Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile	
245 250 255 260	
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC	1110
Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile	
265 270 275	
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG	1158
Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln	
280 285 290	
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC	1206
Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys	
295 300 305	
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA	1254
Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro	
310 315 320	
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC	1302
Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser	
325 330 335 340	
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA	1350
Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser	
345 350 355	
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC	1398
Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr	
360 365 370	

AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC	1446
Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp	
375 380 385	
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG	1494
Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val	
390 395 400	
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC	1542
Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp	
405 410 415 420	
TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG	1590
Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu	
425 430 435	
GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT	1638
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro	
440 445 450	
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG	1686
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met	
455 460 465	
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG	1734
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg	
470 475 480	
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA	1782
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys	
485 490 495 500	
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC	1831
Val Ile Gln	
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG	1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAT	1951
ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA	1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala	
1 5 10 15	
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val	
20 25 30	
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly	
35 40 45	
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln	
50 55 60	
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg	
65 70 75 80	
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn	
85 90 95	
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln	
100 105 110	
Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala	
115 120 125	
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg	
130 135 140	

Arg	Arg	Gln	Glu	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	145	150	155	160
Ser	Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	165	170		175
Leu	Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	180	185		190
Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	195	200		205
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	210	215		220
Ser	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	225	230		240
Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	245	250		255
Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	260	265		270
Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	275	280		285
Leu	Gln	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	290	295		300
Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	305	310		320
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	325	330		335
Leu	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	340	345		350
Val	Met	His	Ser	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro	355	360		365
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln	370	375		380
Ile	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	385	390		400
Phe	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Val	Asn	Gly	405	410		415
Ile	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro	Asn	Asp	420	425		430
Pro	Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	435	440		445
Pro	Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu	450	455		460
Ala	Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu	465	470		480
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Ile	Ser	Asn	Ser	Pro	485	490		495
Glu	Lys	Pro	Lys	Val	Ile	Gln										500			

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG      60
GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA      115
                               Met Val Asp Gly
                               1
GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT      163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
   5                10                15                20
ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG      211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
                25                30                35
TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG      259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
                40                45                50
TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA      307
Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
                55                60                65
GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG      355
Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
   70                75                80
CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC      403
Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
   85                90                95                100
AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA      451
Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
                105                110                115
ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG      499
Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
                120                125                130
TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA      547
Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
                135                140                145
TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT      595
Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
                150                155                160
GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA      643
Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
   165                170                175                180
GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT      691
Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
                185                190                195
CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG      739
Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
                200                205                210
TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA      787
Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln
                215                220                225
GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA      835
Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser
                230                235                240
TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA      883
Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu
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245	AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT	250	255	260	931
	Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser				
	265	270	275		
ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC	979				
Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr					
	280	285	290		
GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA	1027				
Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile					
	295	300	305		
GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT	1075				
Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe					
	310	315	320		
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA	1123				
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys					
	325	330	335	340	
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC	1171				
Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly					
	345	350	355		
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC	1219				
Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn					
	360	365	370		
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT	1267				
Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp					
	375	380	385		
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT	1315				
Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile					
	390	395	400		
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC	1363				
Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser					
	405	410	415	420	
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC	1411				
Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro					
	425	430	435		
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA	1459				
Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln					
	440	445	450		
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC	1507				
Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr					
	455	460	465		
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA	1555				
Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala					
	470	475	480		
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT	1603				
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn					
	485	490	495	500	
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA	1650				
Ser Leu Asp Lys Leu Lys Thr Asp Cys					
505					
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT	1710				
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC	1770				
GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA	1830				
ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA	1890				
AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG	1950				
GCTTTGCATA GCTTTTCAAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT	2010				
GAATTTTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCCTTG	2070				
CATTCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT	2130				

GCGTACTCCA	CTGGTCTGTC	TTTGGATAAT	AGGAATTCAA	TTTGGCAAAA	CAAAATGTAA	2190
TGTCAGACTT	TGCTGCATTT	TACACATGTG	CTGATGTTTA	CAATGATGCC	GAACATTAGG	2250
AATTGTTTTAT	ACACAACTTT	GCAAATTATT	TATTACTTGT	GCACTTAGTA	GTTTTTACAA	2310
AACTGCTTTG	TGCATATGTT	AAAGCTTATT	TTTATGTGGT	CTTATGATTT	TATTACAGAA	2370
ATGTTTTTTAA	CACTATACTC	TAAAATGGAC	ATTTTCTTTT	ATTATCAGTT	AAAATCACAT	2430
TTTAAGTGCT	TCACATTTGT	ATGTGTGTAG	ACTGTAACCT	TTTTTCAGTT	CATATGCAGA	2490
ACGTATTTAG	CCATTACCCA	CGTGACACCA	CCGAATATAT	TATCGATTTA	GAAGCAAAGA	2550
TTTCAGTAGA	ATTTTAGTCC	TGAACGCTAC	GGGGAAAATG	CATTTTCTTC	AGAATTATCC	2610
ATTACGTGCA	TTTAAACTCT	GCCAGAAAAA	AATAACTATT	TTGTTTTAAT	CTACTTTTGT	2670
TATTTAGTAG	TTATTTGTAT	AAATTAAATA	AACTGTTTTT	AAGTCAAAAA	AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu
1				5				10						15	
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu
			20					25						30	
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys
		35					40					45			
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His
	50					55					60				
Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr
65					70					75					80
Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly
			85					90						95	
Asp	Trp	Cys	Asn	Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys
			100					105					110		
Ser	Phe	Pro	Gly	Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile
		115					120					125			
Leu	Ser	Val	Val	Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val
	130					135					140				
Ala	Leu	Arg	Lys	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg
145					150					155				160	
Asp	Val	Glu	Tyr	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly
			165					170					175		
Asp	Ser	Thr	Leu	Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser
		180						185					190		
Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile
	195						200					205			
Thr	Leu	Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg
210						215					220				
Gly	Ser	Trp	Gln	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg
225					230					235				240	
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met
			245						250					255	
Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser
		260						265					270		
Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met
		275					280					285			
Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser
	290					295					300				

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
 305 310 315 320
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
 325 330 335
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
 340 345 350
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
 355 360 365
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
 370 375 380
 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
 385 390 395 400
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
 405 410 415
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
 420 425 430
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
 435 440 445
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
 450 455 460
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
 465 470 475 480
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
 485 490 495
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
 500 505

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT	60
CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA	120
AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG	180
TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA	240
TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC	300
AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC	348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala	
1 5 10	
TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG	396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met	
15 20 25	
CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA	444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu	

30		35		40		45	
AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC	492						
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys							
		50		55		60	
TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA	540						
Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile							
		65		70		75	
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA	588						
Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu							
		80		85		90	
ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG	636						
Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln							
		95		100		105	
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT	684						
Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys							
		110		115		120	
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT	732						
Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val							
		130		135		140	
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC	780						
Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu							
		145		150		155	
ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC	828						
Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys							
		160		165		170	
TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC	876						
Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr							
		175		180		185	
AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA	924						
Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser							
		190		195		200	
CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA	972						
Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly							
		210		215		220	
CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC	1020						
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val							
		225		230		235	
CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG	1068						
Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp							
		240		245		250	
CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC	1116						
Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala							
		255		260		265	
AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT	1164						
Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His							
		270		275		280	
GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC	1212						
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser							
		290		295		300	
TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC	1260						
Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu							
		305		310		315	
TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA	1308						
Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys							
		320		325		330	
TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT	1356						
Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile							

335	340	345	
TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC			1404
Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser			
350	355	360	365
AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG			1452
Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu			
370	375	380	
GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC			1500
Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro			
385	390	395	
TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG			1548
Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu			
400	405	410	
GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC			1596
Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp			
415	420	425	
ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC			1644
Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile			
430	435	440	445
ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA			1692
Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val			
450	455	460	
CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA			1740
Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys			
465	470	475	
CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA			1788
Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu			
480	485	490	
CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC			1836
Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala			
495	500	505	
TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT			1884
Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val			
510	515	520	525
GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAACTCT			1935
Glu Ser Gln Asp Val Lys Ile			
530			
AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT			1995
AACTTGTTTC TCAGACTCTT TCTTCACTAC GTGTTCACAG GCTGCTAATA TTAAACCTTT			2055
CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCAATTCTT TATATATGGA			2115
CAGCTTTATT TTAAATGTGG TTTTGTATGC CTTTTTTTAA GTGGGTTTTT ATGAACTGCA			2175
TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTT			2235
ATAAAACGGT GCTTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA			2295
AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA			2355
GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC			2415
TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTTGA			2475
ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG			2535
CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTACTTTGCA			2595
AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA			2655
AGAAGTTTAA AGCATCTGTA AATTTGGACT TTTTTCCTTC AACCACCATT TTTTTGTGG			2715
TTATTATTTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC			2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG			2835
TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA			2895
TATTTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC			2932

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Thr	Gln	Leu	Tyr	Ile	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Tyr	Leu	Phe
1				5					10					15	
Ile	Ile	Ser	Arg	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly
			20					25					30		
Thr	Gly	Met	Lys	Ser	Asp	Ser	Asp	Gln	Lys	Lys	Ser	Glu	Asn	Gly	Val
		35					40					45			
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser
	50					55					60				
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly
65					70					75					80
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu
				85					90					95	
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp
			100					105					110		
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn
		115					120						125		
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly
	130					135						140			
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met
145					150					155					160
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr
				165					170					175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp
			180					185					190		
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp
		195					200					205			
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu
	210					215						220			
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val
225					230					235					240
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu
				245					250					255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe
			260					265					270		
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile
		275					280					285			
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln
	290					295						300			
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe
305					310					315					320
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr
				325					330					335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr
			340					345					350		
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile
		355					360					365			
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
	370					375					380				
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	Leu	Asn	Thr
385					390					395					400
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser

				405					410					415			
Leu	Asn	Lys	Asn	His	Phe	Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser		
			420					425					430				
Phe	Gly	Leu	Ile	Ile	Trp	Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly		
		435					440					445					
Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp		
	450					455					460						
Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg		
465					470					475					480		
Pro	Ile	Val	Ser	Asn	Arg	Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val		
			485						490					495			
Leu	Lys	Leu	Met	Ser	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu		
		500						505					510				
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln		
	515						520					525					
Asp	Val	Lys	Ile														
	530																

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2333 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG	GCG	GAG	TCG	GCC	GGA	GCC	TCC	TCC	TTC	TTC	CCC	CTT	GTT	GTC	CTC		48
Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu		
1				5					10					15			
CTG	CTC	GCC	GGC	AGC	GGC	GGG	TCC	GGG	CCC	CGG	GGG	GTC	CAG	GCT	CTG		96
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Val	Gln	Ala	Leu		
		20				25					30						
CTG	TGT	GCG	TGC	ACC	AGC	TGC	CTC	CAG	GCC	AAC	TAC	ACG	TGT	GAG	ACA		144
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Ala	Asn	Tyr	Thr	Cys	Glu	Thr		
	35					40				45							
GAT	GGG	GCC	TGC	ATG	GTT	TCC	TTT	TTC	AAT	CTG	GAT	GGG	ATG	GAG	CAC		192
Asp	Gly	Ala	Cys	Met	Val	Ser	Phe	Phe	Asn	Leu	Asp	Gly	Met	Glu	His		
	50					55				60							
CAT	GTG	CGC	ACC	TGC	ATC	CCC	AAA	GTG	GAG	CTG	GTC	CCT	GCC	GGG	AAG		240
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys		
	65				70				75					80			
CCC	TTC	TAC	TGC	CTG	AGC	TCG	GAG	GAC	CTG	CGC	AAC	ACC	CAC	TGC	TGC		288
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys		
		85				90						95					
TAC	ACT	GAC	TAC	TGC	AAC	AGG	ATC	GAC	TTG	AGG	GTG	CCC	AGT	GGT	CAC		336
Tyr	Thr	Asp	Tyr	Cys	Asn	Arg	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His		
	100					105						110					
CTC	AAG	GAG	CCT	GAG	CAC	CCG	TCC	ATG	TGG	GGC	CCG	GTG	GAG	CTG	GTA		384

Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val		
		115					120					125					
GGC	ATC	ATC	GCC	GGC	CCG	GTG	TTC	CTC	CTG	TTC	CTC	ATC	ATC	ATC	ATT	432	
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile		
		130					135					140					
GTT	TTC	CTT	GTC	ATT	AAC	TAT	CAT	CAG	CGT	GTC	TAT	CAC	AAC	CGC	CAG	480	
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln		
		145				150					155				160		
AGA	CTG	GAC	ATG	GAA	GAT	CCC	TCA	TGT	GAG	ATG	TGT	CTC	TCC	AAA	GAC	528	
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp		
				165					170					175			
AAG	ACG	CTC	CAG	GAT	CTT	GTC	TAC	GAT	CTC	TCC	ACC	TCA	GGG	TCT	GGC	576	
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly		
			180						185				190				
TCA	GGG	TTA	CCC	CTC	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	ACC	ATC	GTT	624	
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val		
		195					200					205					
TTA	CAA	GAG	ATT	ATT	GGC	AAG	GGT	CGG	TTT	GGG	GAA	GTA	TGG	CGG	GGC	672	
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly		
		210				215					220						
CGC	TGG	AGG	GGT	GGT	GAT	GTG	GCT	GTG	AAA	ATA	TTC	TCT	TCT	CGT	GAA	720	
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu		
					230					235					240		
GAA	CGG	TCT	TGG	TTC	AGG	GAA	GCA	GAG	ATA	TAC	CAG	ACG	GTC	ATG	CTG	768	
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu		
				245					250					255			
CGC	CAT	GAA	AAC	ATC	CTT	GGA	TTT	ATT	GCT	GCT	GAC	AAT	AAA	GAT	AAT	816	
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn		
			260					265					270				
GGC	ACC	TGG	ACA	CAG	CTG	TGG	CTT	TCT	GAC	TAT	CAT	GAG	CAC	GGG		864	
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly		
		275					280					285					
TCC	CTG	TTT	GAT	TAT	CTG	AAC	CGG	TAC	ACA	GTG	ACA	ATT	GAG	GGG	ATG	912	
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met		
		290				295					300						
ATT	AAG	CTG	GCC	TTG	TCT	GCT	GCT	AGT	GGG	CTG	GCA	CAC	CTG	CAC	ATG	960	
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met		
					310					315					320		
GAG	ATC	GTG	GGC	ACC	CAA	GGG	AAG	CCT	GGA	ATT	GCT	CAT	CGA	GAC	TTA	1008	
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu		
				325					330					335			
AAG	TCA	AAG	AAC	ATT	CTG	GTG	AAG	AAA	AAT	GGC	ATG	TGT	GCC	ATA	GCA	1056	
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala		
			340					345					350				
GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCA	GTC	ACT	GAC	ACC	ATT	GAC	1104	
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp		
		355					360					365					
ATT	GCC	CCG	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	GCC	CCT	GAA	1152	
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu		
		370				375					380						
GTA	CTT	GAT	GAA	ACC	ATT	AAT	ATG	AAA	CAC	TTT	GAC	TCC	TTT	AAA	TGT	1200	
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys		
		385				390				395					400		
GCT	GAT	ATT	TAT	GCC	CTC	GGG	CTT	GTA	TAT	TGG	GAG	ATT	GCT	CGA	AGA	1248	
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg		
				405					410					415			
TGC	AAT	TCT	GGA	GGA	GTC	CAT	GAA	GAA	TAT	CAG	CTG	CCA	TAT	TAC	GAC	1296	

Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	
			420					425					430			
TTA	GTG	CCC	TCT	GAC	CCT	TCC	ATT	GAG	GAA	ATG	CGA	AAG	GTT	GTA	TGT	1344
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	
		435					440					445				
GAT	CAG	AAG	CTG	CGT	CCC	AAC	ATC	CCC	AAC	TGG	TGG	CAG	AGT	TAT	GAG	1392
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu	
		450				455					460					
GCA	CTG	CGG	GTG	ATG	GGG	AAG	ATG	ATG	CGA	GAG	TGT	TGG	TAT	GCC	AAC	1440
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	
		465			470					475				480		
GGC	GCA	GCC	CGC	CTG	ACG	GCC	CTG	CGC	ATC	AAG	AAG	ACC	CTC	TCC	CAG	1488
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln	
			485					490					495			
CTC	AGC	GTG	CAG	GAA	GAC	GTG	AAG	ATC	TA	ACTGCTCC	CTCTCTCCAC					1535
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile								
		500					505									
ACGGAGCTCC	TGGCAGCGAG	AACTACGCAC	AGCTGCCGCG	TTGAGCGTAC	GATGGAGGCC											1595
TACCTCTCGT	TTCTGCCCAG	CCCTCTGTGG	CCAGGAGCCC	TGGCCCAGCA	GAGGGACAGA											1655
GCCCGGGAGA	GACTCGCTCA	CTCCCATGTT	GGGTTTGAGA	CAGACACCTT	TTCTATTTAC											1715
CTCCTAATGG	CATGGAGACT	CTGAGAGCGA	ATTGTGTGGA	GA	ACTCAGTG	CCACACCTCG										1775
AACTGGTTGT	AGTGGGAAGT	CCCGCGAAAC	CCGGTGCATC	TGGCACGTGG	CCAGGAGCCA											1835
TGACAGGGGC	GCTTGGGAGG	GGCCGGAGGA	ACCGAGGTGT	TGCCAGTGCT	AAGCTGCCCT											1895
GAGGGTTTCC	TTCGGGGACC	AGCCACAGC	ACACCAAGGT	GGCCCGGAAG	AACCAGAAGT											1955
GCAGCCCTC	TCACAGGCAG	CTCTGAGCCG	CGCTTTCCCC	TCCTCCCTGG	GATGGACGCT											2015
GCCGGGAGAC	TGCCAGTGGA	GACGGAATCT	GCCGCTTTGT	CTGTCCAGCC	GTGTGTGCAT											2075
GTGCCGAGGT	GCGTCCCCCG	TTGTGCCTGG	TTCTGTGCCAT	GCCCTTACAC	GTGCGTGTGA											2135
GTGTGTGTGT	GTGTCTGTAG	GTGCGCACTT	ACCTGCTTGA	GCTTTCTGTG	CATGTGCAGG											2195
TCGGGGGTGT	GGTCGTCATG	CTGTCCGTGC	TTGCTGGTGC	CTCTTTTCAG	TAGTGAGCAG											2255
CATCTAGTTT	CCCTGGTGCC	CTTCCCTGGA	GGTCTCTCCC	TCCCCCAGAG	CCCCTCATGC											2315
CACAGTGGTA	CTCTGTGT															2333

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu	
1				5					10					15		
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Val	Gln	Ala	Leu	
			20					25					30			
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Ala	Asn	Tyr	Thr	Cys	Glu	Thr	
		35					40					45				
Asp	Gly	Ala	Cys	Met	Val	Ser	Phe	Phe	Asn	Leu	Asp	Gly	Met	Glu	His	
	50					55					60					
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys	
	65				70					75					80	
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys	
			85					90						95		
Tyr	Thr	Asp	Tyr	Cys	Asn	Arg	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His	
		100						105					110			
Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val	
		115					120					125				
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile	

130		135		140
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln				
145		150		155
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp				
	165		170	175
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly				
	180		185	190
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val				
195		200		205
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly				
210		215		220
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu				
225		230		235
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu				
	245		250	255
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn				
	260		265	270
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly				
275		280		285
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met				
290		295		300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met				
305		310		315
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu				
	325		330	335
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala				
	340		345	350
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp				
355		360		365
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu				
370		375		380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys				
385		390		395
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg				
	405		410	415
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp				
	420		425	430
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys				
435		440		445
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu				
450		455		460
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn				
465		470		475
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln				
	485		490	495
Leu Ser Val Gln Glu Asp Val Lys Ile				
500		505		

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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GGCGAGGCGA GGTTTGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG      60
CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG      109
      Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg
              1              5              10
CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG CTG      157
Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Leu
              15              20              25
CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA      205
Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys
              30              35              40
GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA      253
Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr
              45              50              55
GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT      301
Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile
              60              65              70              75
GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA      349
Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys
              80              85              90
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT      397
Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn
              95              100              105
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT      445
Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro
              110              115              120
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC      493
Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile
              125              130              135
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC      541
Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His
              140              145              150              155
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT      589
His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile
              160              165              170
TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA      637
Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser
              175              180              185
GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA      685
Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg
              190              195              200
ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT      733
Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val
              205              210              215
TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC      781
Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser
              220              225              230              235
TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT      829
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr
              240              245              250
GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT      877
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Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn		
			255					260				265					
AAA	GAC	AAT	GGT	ACT	TGG	ACT	CAG	CTC	TGG	TTG	GTG	TCA	GAT	TAT	CAT	925	
Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His		
		270					275				280						
GAG	CAT	GGA	TCC	CTT	TTT	GAT	TAC	TTA	AAC	AGA	TAC	ACA	GTT	ACT	GTG	973	
Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val		
	285					290				295							
GAA	GGA	ATG	ATA	AAA	CTT	GCT	CTG	TCC	ACG	GCG	AGC	GGT	CTT	GCC	CAT	1021	
Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His		
300				305					310					315			
CTT	CAC	ATG	GAG	ATT	GTT	GGT	ACC	CAA	GGA	AAG	CCA	GCC	ATT	GCT	CAT	1069	
Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His		
			320					325			330						
AGA	GAT	TTG	AAA	TCA	AAG	AAT	ATC	TTG	GTA	AAG	AAG	AAT	GGA	ACT	TGC	1117	
Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys		
		335						340				345					
TGT	ATT	GCA	GAC	TTA	GGA	CTG	GCA	GTA	AGA	CAT	GAT	TCA	GCC	ACA	GAT	1165	
Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp		
	350					355					360						
ACC	ATT	GAT	ATT	GCT	CCA	AAC	CAC	AGA	GTG	GGA	ACA	AAA	AGG	TAC	ATG	1213	
Thr	Ile	Asp	Ile	Ala	Pro	Asn	His	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met		
	365					370					375						
GCC	CCT	GAA	GTT	CTC	GAT	GAT	TCC	ATA	AAT	ATG	AAA	CAT	TTT	GAA	TCC	1261	
Ala	Pro	Glu	Val	Leu	Asp	Asp	Ser	Ile	Asn	Met	Lys	His	Phe	Glu	Ser		
380					385				390					395			
TTC	AAA	CGT	GCT	GAC	ATC	TAT	GCA	ATG	GGC	TTA	GTA	TTC	TGG	GAA	ATT	1309	
Phe	Lys	Arg	Ala	Asp	Ile	Tyr	Ala	Met	Gly	Leu	Val	Phe	Trp	Glu	Ile		
		400						405				410					
GCT	CGA	CGA	TGT	TCC	ATT	GGT	GGA	ATT	CAT	GAA	GAT	TAC	CAA	CTG	CCT	1357	
Ala	Arg	Arg	Cys	Ser	Ile	Gly	Gly	Ile	His	Glu	Asp	Tyr	Gln	Leu	Pro		
		415						420				425					
TAT	TAT	GAT	CTT	GTA	CCT	TCT	GAC	CCA	TCA	GTT	GAA	GAA	ATG	AGA	AAA	1405	
Tyr	Tyr	Asp	Leu	Val	Pro	Ser	Asp	Pro	Ser	Val	Glu	Glu	Met	Arg	Lys		
		430					435				440						
GTT	GTT	TGT	GAA	CAG	AAG	TTA	AGG	CCA	AAT	ATC	CCA	AAC	AGA	TGG	CAG	1453	
Val	Val	Cys	Glu	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Gln		
	445					450					455						
AGC	TGT	GAA	GCC	TTG	AGA	GTA	ATG	GCT	AAA	ATT	ATG	AGA	GAA	TGT	TGG	1501	
Ser	Cys	Glu	Ala	Leu	Arg	Val	Met	Ala	Lys	Ile	Met	Arg	Glu	Cys	Trp		
460					465				470					475			
TAT	GCC	AAT	GGA	GCA	GCT	AGG	CTT	ACA	GCA	TTG	CGG	ATT	AAG	AAA	ACA	1549	
Tyr	Ala	Asn	Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr		
			480					485				490					
TTA	TCG	CAA	CTC	AGT	CAA	CAG	GAA	GGC	ATC	AAA	ATG	TAATTCTACA				1595	
Leu	Ser	Gln	Leu	Ser	Gln	Gln	Glu	Gly	Ile	Lys	Met						
		495						500									
GCTTTG	CCCTG	AACTCT	CCTT	TTTTCT	TCAG	ATCTG	CTCCT	GGGTTTT	AAT	TTGGG	GAGGTC					1655	
AGTTGT	TCTA	CCTCACT	AGAG	AGGGAAC	AGAG	AGGATATT	GC	TTCCTTTT	GC	AGCAGT	GTAA					1715	
TAAAGT	CAAT	TAAAACTT	C	CCAGGATT	TT	TTTGGAC	CCA	GGAAAC	AGCC	ATGTGGG	TCC					1775	
TTTCTGT	GCA	CTATGA	ACGC	TTCTTT	TCCA	GGACAG	AAAA	TGTGTAG	TCT	ACCTTT	TATTT					1835	
TTTATTA	ACA	AAACTT	GT	TTTAAAA	AGA	TGATTG	CTGG	TCTTAA	CTTT	AGGTA	ACTCT					1895	
GCTGTG	CTGG	AGATCAT	CTT	TAAGGG	CAAA	GGAGTT	GGAT	TGCTGA	AATTA	CAATGA	AAACA					1955	
TGTCTT	TATTA	CTAAAG	AAAG	TGATTT	ACTC	CTGGTT	AGTA	CATTCT	CAGA	GGATT	CTGAA					2015	
CCACTAG	AGT	TTCCTT	GATT	CAGACT	TTGA	ATGTACT	GT	CTATAG	TTTT	TCAGG	ATCTT					2075	
AAAACTA	ACA	CTTATA	AAAC	TCTTAT	CTTG	AGTCTA	AAAA	TGACCT	CATA	TAGTAG	TGAG					2135	
GAACATA	AATT	CATGCA	AATTG	TATTTT	GTAT	ACTATT	TATTG	TTCTTT	CACT	TATTC	AGAAC					2195	

ATTACATGCC TTCAAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTTCT 2255
AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT 2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg	Leu	Leu	Leu	Val	1	5	10	15
Leu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Pro	Gly	Ala	Thr	20	25	30
Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	Asp	Asn	Phe	Thr	Cys	35	40	45
Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	Glu	Thr	Thr	Asp	Lys	50	55	60
Val	Ile	His	Asn	Ser	Met	Cys	Ile	Ala	Glu	Ile	Asp	Leu	Ile	Pro	Arg	65	70	75
Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	Thr	Gly	Ser	Val	Thr	85	90	95
Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	Lys	Ile	Glu	Leu	Pro	100	105	110
Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	Val	Glu	Leu	Ala	Ala	115	120	125
Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	Ser	Leu	Met	Leu	Met	130	135	140
Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	His	Arg	Val	Pro	Asn	145	150	155
Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	Ser	Glu	Gly	Thr	Thr	165	170	175
Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	Gly	Ser	Gly	Ser	Gly	180	185	190
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	Thr	Ile	Val	Leu	Gln	195	200	205
Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	Lys	Trp	210	215	220
Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	Glu	Arg	225	230	235
Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	Arg	His	245	250	255
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	Gly	Thr	260	265	270
Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	Ser	Leu	275	280	285
Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	Glu	Gly	Met	Ile	Lys	290	295	300
Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	Glu	Ile	305	310	315
Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	325	330	335
Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	340	345	350
Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	Thr	Ile	Asp	Ile	Ala	355	360	365

Pro	Asn	His	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu
370						375					380				
Asp	Asp	Ser	Ile	Asn	Met	Lys	His	Phe	Glu	Ser	Phe	Lys	Arg	Ala	Asp
385				390						395					400
Ile	Tyr	Ala	Met	Gly	Leu	Val	Phe	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Ser
			405						410					415	
Ile	Gly	Gly	Ile	His	Glu	Asp	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	Leu	Val
			420					425					430		
Pro	Ser	Asp	Pro	Ser	Val	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	Glu	Gln
		435						440					445		
Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Gln	Ser	Cys	Glu	Ala	Leu
	450					455					460				
Arg	Val	Met	Ala	Lys	Ile	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	Gly	Ala
465					470					475					480
Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln	Leu	Ser
				485					490					495	
Gln	Gln	Glu	Gly	Ile	Lys	Met									
			500												

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG	CCCTTCCCAG	TCCCCGGAGC	CGCCGCGCCA	CGCGCGCATG	ATCAAGACCT	60
TTTCCCCGGC	CCCACAGGGC	CTCTGGACGT	GAGACCCCGG	CCGCCTCCGC	AAGGAGAGGC	120
GGGGGTCGAG	TCGCCCTGTC	CAAAGGCCTC	AATCTAAACA	ATCTTGATTC	CTGTTGCCGG	180
CTGGCGGGAC	CCTGAATGGC	AGGAAATCTC	ACCACATCTC	TTCTCCTATC	TCCAAGGACC	240
ATG ACC TTG	GGG AGC TTC	AGA AGG GGC	CTT TTG	ATG CTG	TCG GTG GCC	288
Met Thr Leu	Gly Ser Phe	Arg Arg Gly	Leu Leu Met	Leu Ser	Val Ala	
1	5	10	15			
TTG GGC CTA	ACC CAG GGG	AGA CTT GCG	AAG CCT TCC	AAG CTG	GTG AAC	336
Leu Gly Leu	Thr Gln Gly	Arg Leu Ala	Lys Pro Ser	Lys Leu	Val Asn	
	20	25	30			
TGC ACT TGT	GAG AGC CCA	CAC TGC AAG	AGA CCA TTC	TGC CAG	GGG TCA	384
Cys Thr Cys	Glu Ser Pro	His Cys Lys	Arg Pro Phe	Cys Gln	Gly Ser	
	35	40	45			
TGG TGC ACA	GTG GTG CTG	GTT CGA GAG	CAG GGC AGG	CAC CCC	CAG GTC	432
Trp Cys Thr	Val Val Leu	Val Arg Glu	Gln Gly Arg	His Pro	Gln Val	
	50	55	60			
TAT CGG GGC	TGT GGG AGC	CTG AAC CAG	GAG CTC TGC	TTG GGA	CGT CCC	480
Tyr Arg Gly	Cys Gly Ser	Leu Asn Gln	Glu Leu Cys	Leu Gly	Arg Pro	
	65	70	75		80	
ACG GAG TTT	CTG AAC CAT	CAC TGC TGC	TAT AGA TCC	TTC TGC	AAC CAC	528
Thr Glu Phe	Leu Asn His	His Cys Cys	Tyr Arg Ser	Phe Cys	Asn His	

				85				90					95				
AAC	GTG	TCT	CTG	ATG	CTG	GAG	GCC	ACC	CAA	ACT	CCT	TCG	GAG	GAG	CCA		576
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro		
			100					105					110				
GAA	GTT	GAT	GCC	CAT	CTG	CCT	CTG	ATC	CTG	GGT	CCT	GTG	CTG	GCC	TTG		624
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu		
			115					120					125				
CCG	GTC	CTG	GTG	GCC	CTG	GGT	GCT	CTG	GGC	TTG	TGG	CGT	GTC	CGG	CGG		672
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg		
			130					135				140					
AGG	CAG	GAG	AAG	CAG	CGG	GAT	TTG	CAC	AGT	GAC	CTG	GGC	GAG	TCC	AGT		720
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser		
			145			150				155					160		
CTC	ATC	CTG	AAG	GCA	TCT	GAA	CAG	GCA	GAC	AGC	ATG	TTG	GGG	GAC	TTC		768
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe		
			165						170					175			
CTG	GAC	AGC	GAC	TGT	ACC	ACG	GGC	AGC	GGC	TCG	GGG	CTC	CCC	TTC	TTG		816
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu		
			180					185					190				
GTG	CAG	AGG	ACG	GTA	GCT	CGG	CAG	GTT	GCG	CTG	GTA	GAG	TGT	GTG	GGA		864
Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly		
			195					200					205				
AAG	GGC	CGA	TAT	GGC	GAG	GTG	TGG	CGC	GGT	TCG	TGG	CAT	GGC	GAA	AGC		912
Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser		
			210			215					220						
GTG	GCG	GTC	AAG	ATT	TTC	TCC	TCA	CGA	GAT	GAG	CAG	TCC	TGG	TTC	CGG		960
Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg		
			225		230					235				240			
GAG	ACG	GAG	ATC	TAC	AAC	ACA	GTT	CTG	CTT	AGA	CAC	GAC	AAC	ATC	CTA		1008
Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu		
			245						250					255			
GGC	TTC	ATC	GCC	TCC	GAC	ATG	ACT	TCG	CGG	AAC	TCG	AGC	ACG	CAG	CTG		1056
Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu		
			260					265					270				
TGG	CTC	ATC	ACC	CAC	TAC	CAT	GAA	CAC	GGC	TCC	CTC	TAT	GAC	TTT	CTG		1104
Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu		
			275				280						285				
CAG	AGG	CAG	ACG	CTG	GAG	CCC	CAG	TTG	GCC	CTG	AGG	CTA	GCT	GTG	TCC		1152
Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser		
			290			295					300						
CCG	GCC	TGC	GGC	CTG	GCG	CAC	CTA	CAT	GTG	GAG	ATC	TTT	GGC	ACT	CAA		1200
Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln		
			305			310				315				320			
GGC	AAA	CCA	GCC	ATT	GCC	CAT	CGT	GAC	CTC	AAG	AGT	CGC	AAT	GTG	CTG		1248
Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu		
			325						330					335			
GTC	AAG	AGT	AAC	TTG	CAG	TGT	TGC	ATT	GCA	GAC	CTG	GGA	CTG	GCT	GTG		1296
Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val		
			340					345					350				
ATG	CAC	TCA	CAA	AGC	AAC	GAG	TAC	CTG	GAT	ATC	GGC	AAC	ACA	CCC	CGA		1344
Met	His	Ser	Gln	Ser	Asn	Glu	Tyr	Leu	Asp	Ile	Gly	Asn	Thr	Pro	Arg		
			355				360						365				
GTG	GGT	ACC	AAA	AGA	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAT	GAG	CAC	ATC		1392
Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	His	Ile		
			370			375					380						
CGC	ACA	GAC	TGC	TTT	GAG	TCG	TAC	AAG	TGG	ACA	GAC	ATC	TGG	GCC	TTT		1440
Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe		

385		390		395		400	
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT							1488
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile							
	405		410		415		
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC							1536
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro							
	420		425		430		
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC							1584
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro							
	435		440		445		
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC							1632
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala							
	450		455		460		
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC							1680
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr							
	465		470		475		480
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG							1728
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu							
	485		490		495		
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT							1776
Lys Pro Lys Val Ile His							
	500						
AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA AGAGAGTGTG							1836
CACGCTGCCC TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC							1896
TGAGCTGAAA TTCAAAAAA AAAAAA							1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Thr	Leu	Gly	Ser	Phe	Arg	Arg	Gly	Leu	Leu	Met	Leu	Ser	Val	Ala
1				5					10					15	
Leu	Gly	Leu	Thr	Gln	Gly	Arg	Leu	Ala	Lys	Pro	Ser	Lys	Leu	Val	Asn
			20					25					30		
Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Arg	Pro	Phe	Cys	Gln	Gly	Ser
			35				40					45			
Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Gln	Gly	Arg	His	Pro	Gln	Val
			50			55				60					
Tyr	Arg	Gly	Cys	Gly	Ser	Leu	Asn	Gln	Glu	Leu	Cys	Leu	Gly	Arg	Pro
			65		70				75				80		
Thr	Glu	Phe	Leu	Asn	His	His	Cys	Cys	Tyr	Arg	Ser	Phe	Cys	Asn	His
				85					90				95		
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro
			100					105					110		
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu
			115				120					125			
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg
			130			135					140				
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser
			145		150				155				160		
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe
			165				170					175			
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu

(B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTTCATGAGA	TGGAAGCATA	GGTCAAAGCT	GTTCGGAGAA	ATTGGAACATA	CAGTTTTATC	60										
TAGCCACATC	TCTGAGAATT	CTGAAGAAAG	CAGCAGGTGA	AAGTCATTGC	CAAGTGATTT	120										
TGTTCTGTAA	GGAAGCCTCC	CTCATTCACT	TACACCAGTG	AGACAGCAGG	ACCAGTCATT	180										
CAAAGGGCCG	TGTACAGGAC	GCGTGGCAAT	CAGACA	ATG	ACT CAG CTA TAC ACT	234										
			Met	Thr	Gln Leu Tyr Thr											
			1		5											
TAC	ATC	AGA	TTA	CTG	GGA	GCC	TGT	CTG	TTC	ATC	ATT	TCT	CAT	GTT	CAA	282
Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe	Ile	Ile	Ser	His	Val	Gln	
		10						15					20			
GGG	CAG	AAT	CTA	GAT	AGT	ATG	CTC	CAT	GGC	ACT	GGT	ATG	AAA	TCA	GAC	330
Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly	Thr	Gly	Met	Lys	Ser	Asp	
		25					30					35				
TTG	GAC	CAG	AAG	AAG	CCA	GAA	AAT	GGA	GTG	ACT	TTA	GCA	CCA	GAG	GAT	378
Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val	Thr	Leu	Ala	Pro	Glu	Asp	
	40					45					50					
ACC	TTG	CCT	TTC	TTA	AAG	TGC	TAT	TGC	TCA	GGA	CAC	TGC	CCA	GAT	GAT	426
Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	Gly	His	Cys	Pro	Asp	Asp	
	55				60					65				70		
GCT	ATT	AAT	AAC	ACA	TGC	ATA	ACT	AAT	GGC	CAT	TGC	TTT	GCC	ATT	ATA	474
Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	His	Cys	Phe	Ala	Ile	Ile	
				75				80					85			
GAA	GAA	GAT	GAT	CAG	GGA	GAA	ACC	ACA	TTA	ACT	TCT	GGG	TGT	ATG	AAG	522
Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	Thr	Ser	Gly	Cys	Met	Lys	
		90					95					100				
TAT	GAA	GGC	TCT	GAT	TTT	CAA	TGC	AAG	GAT	TCA	CCG	AAA	GCC	CAG	CTA	570
Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	Ser	Pro	Lys	Ala	Gln	Leu	
	105						110					115				
CGC	AGG	ACA	ATA	GAA	TGT	TGT	CGG	ACC	AAT	TTG	TGC	AAC	CAG	TAT	TTG	618
Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	Leu	Cys	Asn	Gln	Tyr	Leu	
	120				125						130					
CAG	CCT	ACA	CTG	CCC	CCT	GTT	GTT	ATA	GGT	CCG	TTC	TTT	GAT	GGC	AGC	666
Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser	
	135				140				145					150		
ATC	CGA	TGG	CTG	GTT	GTG	CTC	ATT	TCC	ATG	GCT	GTC	TGT	ATA	GTT	GCT	714
Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met	Ala	Val	Cys	Ile	Val	Ala	
			155					160					165			
ATG	ATC	ATC	TTC	TCC	AGC	TGC	TTT	TGC	TAT	AAG	CAT	TAT	TGT	AAG	AGT	762
Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser	
		170					175					180				
ATC	TCA	AGC	AGG	GGT	CGT	TAC	AAC	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	810
Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala	
		185					190					195				
TTT	ATT	CCA	GTA	GGA	GAA	TCA	TTG	AAA	GAC	CTG	ATT	GAC	CAG	TCC	CAA	858
Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	
	200					205					210					
AGC	TCT	GGG	AGT	GGA	TCT	GGA	TTG	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	906
Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	
	215				220					225				230		
GCC	AAA	CAG	ATT	CAG	ATG	GTT	CGG	CAG	GTT	GGT	AAA	GGC	CGC	TAT	GGA	954
Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	
			235					240				245				
GAA	GTA	TGG	ATG	GGT	AAA	TGG	CGT	GGT	GAA	AAA	GTG	GCT	GTC	AAA	GTG	1002
Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	
		250					255					260				
TTT	TTT	ACC	ACT	GAA	GAA	GCT	AGC	TGG	TTT	AGA	GAA	ACA	GAA	ATC	TAC	1050

Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	
	265						270				275					
CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	CTT	GGT	TTT	ATA	GCT	GCA	1098
Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	
	280						285				290					
GAC	ATT	AAA	GGC	ACT	GGT	TCC	TGG	ACT	CAG	CTG	TAT	TTG	ATT	ACT	GAT	1146
Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	
295					300					305					310	
TAC	CAT	GAA	AAT	GGA	TCT	CTC	TAT	GAC	TTC	CTG	AAA	TGT	GCC	ACA	CTA	1194
Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu	
			315						320						325	
GAC	ACC	AGA	GCC	CTA	CTC	AAG	TTA	GCT	TAT	TCT	GCT	GCT	TGT	GGT	CTG	1242
Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu	
			330						335						340	
TGC	CAC	CTC	CAC	ACA	GAA	ATT	TAT	GGT	ACC	CAA	GGG	AAG	CCT	GCA	ATT	1290
Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	
			345						350						355	
GCT	CAT	CGA	GAC	CTG	AAG	AGC	AAA	AAC	ATC	CTT	ATT	AAG	AAA	AAT	GGA	1338
Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly	
			360						365						370	
AGT	TGC	TGT	ATT	GCT	GAC	CTG	GGC	CTA	GCT	GTT	AAA	TTC	AAC	AGT	GAT	1386
Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp	
375					380					385					390	
ACA	AAT	GAA	GTT	GAC	ATA	CCC	TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAG	CGG	1434
Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	
				395					400						405	
TAC	ATG	GCT	CCA	GAA	GTG	CTG	GAT	GAA	AGC	CTG	AAT	AAA	AAC	CAT	TTC	1482
Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe	
			410						415						420	
CAG	CCC	TAC	ATC	ATG	GCT	GAC	ATC	TAT	AGC	TTT	GGT	TTG	ATC	ATT	TGG	1530
Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp	
			425						430						435	
GAA	ATG	GCT	CGT	CGT	TGT	ATT	ACA	GGA	GGA	ATC	GTG	GAG	GAA	TAT	CAA	1578
Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	
			440						445						450	
TTA	CCA	TAT	TAC	AAC	ATG	GTG	CCC	AGT	GAC	CCA	TCC	TAT	GAG	GAC	ATG	1626
Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	
455					460					465					470	
CGT	GAG	GTT	GTG	TGT	GTG	AAA	CGC	TTG	CGG	CCA	ATC	GTG	TCT	AAC	CGC	1674
Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	
				475					480						485	
TGG	AAC	AGC	GAT	GAA	TGT	CTT	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	1722
Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	
			490						495						500	
TGT	TGG	GCC	CAT	AAT	CCA	GCC	TCC	AGA	CTC	ACA	GCT	TTG	AGA	ATC	AAG	1770
Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	
			505						510						515	
AAG	ACA	CTT	GCA	AAA	ATG	GTT	GAA	TCC	CAG	GAT	GTA	AAG	ATT			1812
Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln	Asp	Val	Lys	Ile			
			520						525						530	
TGACAATTAA	ACAATTTTGA	GGGAGAATTT	AGACTGCAAG	AACCTTCTTCA	CCCAAGGAAT											1872
GGGTGGGATT	AGCATGGAAT	AGGATGTTGA	CTTGGTTTCC	AGACTCCTTC	CTCTACATCT											1932
TCACAGGCTG	CTAACAGTAA	ACCTTACCGT	ACTCTACAGA	ATACAAGATT	GGAACCTGGA											1992
ACTTCAAACA	TGTCATTCTT	TATATATGAC	AGCTTTGTTT	TAATGTGGGG	TTTTTTTGT											2052
TGCTTTTTTT	GTTTTGTT															2070

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Thr	Gln	Leu	Tyr	Thr	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe
1				5					10					15	
Ile	Ile	Ser	His	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly
			20					25					30		
Thr	Gly	Met	Lys	Ser	Asp	Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val
		35					40					45			
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser
	50					55					60				
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly
65					70					75					80
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu
				85					90					95	
Thr	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp
			100					105					110		
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn
		115					120					125			
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly
130						135					140				
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met
145					150					155					160
Ala	Val	Cys	Ile	Val	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr
				165					170					175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp
			180					185					190		
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp
		195					200					205			
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu
210						215					220				
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val
225					230					235					240
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu
				245					250					255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe
			260					265					270		
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile
		275					280					285			
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln
290						295					300				
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe
305					310					315					320
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr
				325					330					335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr
			340					345					350		
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile
		355					360					365			
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
370					375						380				
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr
385					390					395					400

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
405 410 415
Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
420 425 430
Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
435 440 445
Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
450 455 460
Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
465 470 475 480
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
485 490 495
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
500 505 510
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
515 520 525
Asp Val Lys Ile
530

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu	
1 5 10	
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC	96
Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile	
15 20 25	
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC	144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr	
30 35 40 45	
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	

AGC	GGA	CAC	CTC	AAG	GAG	CCT	GCG	CAC	CCC	TCC	ATG	TGG	GGC	CCT	GTG	384
Ser	Gly	His	Leu	Lys	Glu	Pro	Ala	His	Pro	Ser	Met	Trp	Gly	Pro	Val	
110					115					120					125	
GAG	CTG	GTC	GGC	ATC	ATC	GCC	GGC	CCC	GTC	TTC	CTC	CTC	TTC	CTT	ATC	432
Glu	Leu	Val	Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	
				130					135						140	
ATT	ATC	ATC	GTC	TTC	CTG	GTC	ATC	AAC	TAT	CAC	CAG	CGT	GTC	TAC	CAT	480
Ile	Ile	Ile	Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	
			145					150					155			
AAC	CGC	CAG	AGG	TTG	GAC	ATG	GAG	GAC	CCC	TCT	TGC	GAG	ATG	TGT	CTC	528
Asn	Arg	Gln	Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	
		160					165					170				
TCC	AAA	GAC	AAG	ACG	CTC	CAG	GAT	CTC	GTC	TAC	GAC	CTC	TCC	ACG	TCA	576
Ser	Lys	Asp	Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	
	175				180						185					
GGG	TCT	GGC	TCA	GGG	TTA	CCC	CTT	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	624
Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	
190					195					200					205	
ACC	ATT	GTT	TTA	CAA	GAG	ATT	ATC	GGC	AAG	GGC	CGG	TTC	GGG	GAA	GTA	672
Thr	Ile	Val	Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	
				210				215						220		
TGG	CGT	GGT	CGC	TGG	AGG	GGT	GGT	GAC	GTG	GCT	GTG	AAA	ATC	TTC	TCT	720
Trp	Arg	Gly	Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	
		225						230					235			
TCT	CGT	GAA	GAA	CGG	TCT	TGG	TTC	CGT	GAA	GCA	GAG	ATC	TAC	CAG	ACC	768
Ser	Arg	Glu	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	
		240					245					250				
GTC	ATG	CTG	CGC	CAT	GAA	AAC	ATC	CTT	GGC	TTT	ATT	GCT	GCT	GAC	AAT	816
Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	
	255				260						265					
AAA	GAT	AAT	GGC	ACC	TGG	ACC	CAG	CTG	TGG	CTT	GTC	TCT	GAC	TAT	CAC	864
Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	
270					275					280					285	
GAG	CAT	GGC	TCA	CTG	TTT	GAT	TAT	CTG	AAC	CGC	TAC	ACA	GTG	ACC	ATT	912
Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	
				290				295						300		
GAG	GGA	ATG	ATT	AAG	CTA	GCC	TTG	TCT	GCA	GCC	AGT	GGT	TTG	GCA	CAC	960
Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	
				305				310					315			
CTG	CAT	ATG	GAG	ATT	GTG	GGC	ACT	CAA	GGG	AAG	CCG	GGA	ATT	GCT	CAT	1008
Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	
		320					325					330				
CGA	GAC	TTG	AAG	TCA	AAG	AAC	ATC	CTG	GTG	AAA	AAA	AAT	GGC	ATG	TGT	1056
Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	
	335					340					345					
GCC	ATT	GCA	GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCG	GTC	ACT	GAC	1104
Ala	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	
350					355					360					365	
ACC	ATA	GAC	ATT	GCT	CCA	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	1152
Thr	Ile	Asp	Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	
				370					375					380		
GCT	CCT	GAA	GTC	CTT	GAC	GAG	ACA	ATC	AAC	ATG	AAG	CAC	TTT	GAC	TCC	1200
Ala	Pro	Glu	Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	
			385					390					395			
TTC	AAA	TGT	GCC	GAC	ATC	TAT	GCC	CTC	GGG	CTT	GTC	TAC	TGG	GAG	ATT	1248
Phe	Lys	Cys	Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	
	400						405					410				

GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG	1296
Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG	1344
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys	
430 435 440 445	
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG	1392
Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln	
450 455 460	
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG	1440
Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp	
465 470 475	
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT	1488
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC	1534
Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile	
495 500 505	
CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT	1594
GGAGGCCTAT CCTCTTGTTT CTGCCCCGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA	1654
CAGAGCCTGG GAGACGCGCG CACTCCCGTT GGGTTTGAGA CAGACACTTT TTATATTTAC	1714
CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC	1774
GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG	1834
CTCGCCAGGA GCGGCCCCCA TACCTTGTTG TCCACTGGGC TGCAGGTTTT CCTCCAGGGA	1894
CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGBAAGT TTCTCCCTCC TTCCCGTAGC	1954
AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCCTA GAGACACAAC	2014
CTGCTGCCCTG TCTGTCCAGC CAAGTGCAGCA TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG	2074
GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACTTAA	2134
ACCTGCTTGA GCTTCTGTGC ATGTGT	2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu
1				5					10					15	
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Ile	Gln	Ala	Leu
			20					25					30		
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Thr	Asn	Tyr	Thr	Cys	Glu	Thr
		35				40					45				
Asp	Gly	Ala	Cys	Met	Val	Ser	Ile	Phe	Asn	Leu	Asp	Gly	Val	Glu	His
	50					55					60				
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys
	65				70					75				80	
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys
				85					90					95	
Tyr	Ile	Asp	Phe	Cys	Asn	Lys	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His
			100					105					110		
Leu	Lys	Glu	Pro	Ala	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
		115					120					125			
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile
	130					135					140				
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln

145		150		155		160
Arg	Leu	Asp	Met	Glu	Asp	Pro
		165		170		175
Lys	Thr	Leu	Gln	Asp	Leu	Val
		180		185		190
Ser	Gly	Leu	Pro	Leu	Phe	Val
		195		200		205
Leu	Gln	Glu	Ile	Ile	Gly	Lys
		210		215		220
Arg	Trp	Arg	Gly	Gly	Asp	Val
		225		230		235
Glu	Arg	Ser	Trp	Phe	Arg	Glu
		245		250		255
Arg	His	Glu	Asn	Ile	Leu	Gly
		260		265		270
Gly	Thr	Trp	Thr	Gln	Leu	Trp
		275		280		285
Ser	Leu	Phe	Asp	Tyr	Leu	Asn
		290		295		300
Ile	Lys	Leu	Ala	Leu	Ser	Ala
		305		310		315
Glu	Ile	Val	Gly	Thr	Gln	Gly
		325		330		335
Lys	Ser	Lys	Asn	Ile	Leu	Val
		340		345		350
Asp	Leu	Gly	Leu	Ala	Val	Arg
		355		360		365
Ile	Ala	Pro	Asn	Gln	Arg	Val
		370		375		380
Val	Leu	Asp	Glu	Thr	Ile	Asn
		385		390		395
Ala	Asp	Ile	Tyr	Ala	Leu	Gly
		405		410		415
Cys	Asn	Ser	Gly	Gly	Val	His
		420		425		430
Leu	Val	Pro	Ser	Asp	Pro	Ser
		435		440		445
Asp	Gln	Lys	Leu	Arg	Pro	Asn
		450		455		460
Ala	Leu	Arg	Val	Met	Gly	Lys
		465		470		475
Gly	Ala	Ala	Arg	Leu	Thr	Ala
		485		490		495
Leu	Ser	Val	Gln	Glu	Asp	Val
		500		505		

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1952 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGCGGC AGAAGTTGCC GGCCTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC	60
TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC	120
AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT	180
GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG	228
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys	
1 5 10	
AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA	276
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu	
15 20 25 30	
CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC	324
Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile	
35 40 45	
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT	372
Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser	
50 55 60	
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT	420
Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp	
65 70 75	
TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA	468
Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu	
80 85 90	
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG	516
Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu	
95 100 105 110	
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG	564
Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys	
115 120 125	
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT	612
Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile	
130 135 140	
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG	660
Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg	
145 150 155	
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG	708
Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu	
160 165 170	
TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA	756
Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser	
175 180 185 190	
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG	804
Gly Leu Pro Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met	
195 200 205	
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG	852
Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys	
210 215 220	
TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA	900
Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu	
225 230 235	
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG	948
Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg	
240 245 250	

CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG	996
His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly	
255 260 265 270	
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC	1044
Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser	
275 280 285	
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG	1092
Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu	
290 295 300	
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA	1140
Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu	
305 310 315	
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA	1188
Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
320 325 330	
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
370 375 380	
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	
385 390 395	
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT	1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys	
400 405 410	
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG	1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu	
415 420 425 430	
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG	1524
Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met	
435 440 445	
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT	1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
450 455 460	
CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT	1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
465 470 475	
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG	1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
480 485 490	
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA	1722
Ser Glu Ser Gln Asp Ile Lys Leu	
495 500	
ATTTCACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA	1782
GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT	1842
CATGGCTTTC TGAGGAGGAG AAAGTGTGTTG GGTAACCTGT TCAAGATATG ATGCATGTTG	1902
CTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTT ATAAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Leu	Leu	Arg	Ser	Ser	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys	Lys	Glu
1				5				10						15	
Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Ile	Leu	Arg	Cys
			20					25					30		
Lys	Cys	His	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser
		35					40				45				
Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	Gly	Met
	50					55					60				
Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln
65					70					75					80
Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	Cys	Cys
				85				90						95	
Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	Pro	Pro
			100					105					110		
Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	Ala	Leu
	115						120				125				
Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	Ile	Leu
	130					135					140				
Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	Tyr	Ser
145					150					155					160
Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	Ser	Leu
				165				170						175	
Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu
		180						185					190		
Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Lys
	195						200					205			
Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg
	210					215					220				
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser
225					230					235					240
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu
				245					250					255	
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp
		260						265					270		
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr
		275					280					285			
Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	Lys	Leu
	290					295					300				
Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Phe
305					310					315					320
Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys
				325					330					335	
Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	Gly
		340					345						350		
Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Pro
	355						360					365			
Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	Leu	Asp
	370					375						380			
Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	Asp	Met
385					390					395					400
Tyr	Ser	Phe	Gly	Leu	Ile	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Val	Ser
				405					410					415	
Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	His	Asp	Leu	Val	Pro

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
CGGAATTCTG GTGCCATATA 20

(2) INFORMATION FOR SEQ ID NO: 23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG 37

(2) INFORMATION FOR SEQ ID NO: 24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
GCGGATCCAC CATGGCGGAG TCGGCC 26

(2) INFORMATION FOR SEQ ID NO: 25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
AACACCGGGC CGGCGATGAT 20

(2) INFORMATION FOR SEQ ID NO: 26:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
Gly Xaa Gly Xaa Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 27:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 Asp Phe Lys Ser Arg Asn
 1 5

(2) INFORMATION FOR SEQ ID NO: 28:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 Asp Leu Lys Ser Lys Asn
 1 5

(2) INFORMATION FOR SEQ ID NO: 29:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 Gly Thr Lys Arg Tyr Met
 1 5

(2) INFORMATION FOR SEQ ID NO: 30:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
 5 10 15
 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
 20 25 30
 Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
 35 40 45
 Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
 50 55 60
 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
 65 70 75 80
 Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
 85 90 95
 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
 100 105 110
 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn

		115					120				125				
Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu
	130					135					140				
Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val
145					150					155					160
Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln
				165					170					175	
Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu
			180					185					190		
Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys
	195					200						205			
Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln
210					215						220				
Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly
225					230					235					240
Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly
				245					250					255	
Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys
			260					265					270		
Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu
	275					280						285			
Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His
290					295						300				
Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His
305					310					315					320
Arg	Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala
				325					330					335	
Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser
			340					345					350		
Ala	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro
	355					360						365			
Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	Phe	Leu	Arg
370					375						380				
Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	Ala	Ser	Arg
385					390					395					400
Cys	Thr	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	Pro	Phe	Glu
				405					410					415	
Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Asp	Met	Gln	Glu	Val	Val
			420					425				430			
Val	His	Lys	Lys	Lys	Arg	Pro	Val	Leu	Arg	Asp	Tyr	Trp	Gln	Lys	His
		435				440						445			
Ala	Gly	Met	Ala	Met	Leu	Cys	Glu	Thr	Ile	Glu	Glu	Cys	Trp	Asp	His
450					455						460				
Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly	Cys	Val	Gly	Glu	Arg	Ile	Thr
465					470					475					480
Gln	Met	Gln	Arg	Leu	Thr	Asn	Ile	Ile	Thr	Thr	Glu	Asp	Ile	Val	Thr
				485					490					495	
Val	Val	Thr	Met	Val	Thr	Asn	Val	Asp	Phe	Pro	Pro	Lys	Glu	Ser	Ser
			500					505					510		
Leu															

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met	Thr	Ala	Pro	Trp	Ala	Ala	Leu	Ala	Leu	Leu	Trp	Gly	Ser	Leu	Cys
			5						10					15	
Ala	Gly	Ser	Gly	Arg	Gly	Glu	Ala	Glu	Thr	Arg	Glu	Cys	Ile	Tyr	Tyr
			20					25					30		
Asn	Ala	Asn	Trp	Glu	Leu	Glu	Arg	Thr	Asn	Gln	Ser	Gly	Leu	Glu	Arg
			35				40					45			
Cys	Glu	Gly	Glu	Gln	Asp	Lys	Arg	Leu	His	Cys	Tyr	Ala	Ser	Trp	Arg
			50			55					60				
Asn	Ser	Ser	Gly	Thr	Ile	Glu	Leu	Val	Lys	Lys	Gly	Cys	Trp	Leu	Asp
65					70					75				80	
Asp	Phe	Asn	Cys	Tyr	Asp	Arg	Gln	Glu	Cys	Val	Ala	Thr	Glu	Glu	Asn
			85					90					95		
Pro	Gln	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Phe	Cys	Asn	Glu	Arg
			100					105					110		
Phe	Thr	His	Leu	Pro	Glu	Pro	Gly	Gly	Pro	Glu	Val	Thr	Tyr	Glu	Pro
			115				120					125			
Pro	Pro	Thr	Ala	Pro	Thr	Leu	Leu	Thr	Val	Leu	Ala	Tyr	Ser	Leu	Leu
			130			135					140				
Pro	Ile	Gly	Gly	Leu	Ser	Leu	Ile	Val	Leu	Leu	Ala	Phe	Trp	Met	Tyr
145					150					155				160	
Arg	His	Arg	Lys	Pro	Pro	Tyr	Gly	His	Val	Asp	Ile	His	Glu	Val	Arg
			165					170					175		
Gln	Cys	Gln	Arg	Trp	Ala	Gly	Arg	Arg	Asp	Gly	Cys	Ala	Asp	Ser	Phe
			180				185					190			
Lys	Pro	Leu	Pro	Phe	Gln	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu
		195				200					205				
Val	Gly	Leu	Lys	Pro	Leu	Gln	Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg
	210				215					220					
Phe	Gly	Cys	Val	Trp	Lys	Ala	Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val
225				230					235					240	
Lys	Ile	Phe	Pro	Leu	Gln	Asp	Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu
			245					250					255		
Ile	Phe	Ser	Thr	Pro	Gly	Met	Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile
			260			265							270		
Ala	Ala	Glu	Lys	Arg	Gly	Ser	Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile
		275				280					285				
Thr	Ala	Phe	His	Asp	Lys	Gly	Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn
	290				295					300					
Ile	Ile	Thr	Trp	Asn	Glu	Leu	Cys	His	Val	Ala	Glu	Thr	Met	Ser	Arg
305				310					315					320	
Gly	Leu	Ser	Tyr	Leu	His	Glu	Asp	Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly
			325					330					335		
His	Lys	Pro	Ser	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu
		340				345						350			
Leu	Lys	Ser	Asp	Leu	Thr	Ala	Val	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val
	355				360					365					
Arg	Phe	Glu	Pro	Gly	Lys	Pro	Pro	Gly	Asp	Thr	His	Gly	Gln	Val	Gly
	370				375					380					
Thr	Arg	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe
385				390					395					400	
Gln	Arg	Asp	Ala	Phe	Leu	Arg	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val
			405				410						415		
Leu	Trp	Glu	Leu	Val	Ser	Arg	Cys	Lys	Ala	Ala	Asp	Gly	Pro	Val	Asp
		420				425						430			
Glu	Tyr	Met	Leu	Pro	Phe	Glu	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu

		435					440				445					
Glu	Glu	Leu	Gln	Glu	Val	Val	Val	His	Lys	Lys	Met	Arg	Pro	Thr	Ile	
	450						455				460					
Lys	Asp	His	Trp	Leu	Lys	His	Pro	Gly	Leu	Ala	Gln	Leu	Cys	Val	Thr	
465					470					475					480	
Ile	Glu	Glu	Cys	Trp	Asp	His	Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly	
				485					490					495		
Cys	Val	Glu	Glu	Arg	Val	Ser	Leu	Ile	Arg	Arg	Ser	Val	Asn	Gly	Thr	
		500					505					510				
Thr	Ser	Asp	Cys	Leu	Val	Ser	Leu	Val	Thr	Ser	Val	Thr	Asn	Val	Asp	
	515					520						525				
Leu	Leu	Pro	Lys	Glu	Ser	Ser	Ile									
	530					535										

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Gly	Arg	Gly	Leu	Leu	Arg	Gly	Leu	Trp	Pro	Leu	His	Ile	Val	Leu	
			5					10						15		
Trp	Thr	Arg	Ile	Ala	Ser	Thr	Ile	Pro	Pro	His	Val	Gln	Lys	Ser	Val	
		20					25					30				
Asn	Asn	Asp	Met	Ile	Val	Thr	Asp	Asn	Asn	Gly	Ala	Val	Lys	Phe	Pro	
	35					40					45					
Gln	Leu	Cys	Lys	Phe	Cys	Asp	Val	Arg	Phe	Ser	Thr	Cys	Asp	Asn	Gln	
	50				55					60						
Lys	Ser	Cys	Met	Ser	Asn	Cys	Ser	Ile	Thr	Ser	Ile	Cys	Glu	Lys	Pro	
65				70				75						80		
Gln	Glu	Val	Cys	Val	Ala	Val	Trp	Arg	Lys	Asn	Asp	Glu	Asn	Ile	Thr	
			85				90							95		
Leu	Glu	Thr	Val	Cys	His	Asp	Pro	Lys	Leu	Pro	Tyr	His	Asp	Phe	Ile	
		100					105					110				
Leu	Glu	Asp	Ala	Ala	Ser	Pro	Lys	Cys	Ile	Met	Lys	Glu	Lys	Lys	Lys	
	115					120					125					
Pro	Gly	Glu	Thr	Phe	Phe	Met	Cys	Ser	Cys	Ser	Ser	Asp	Glu	Cys	Asn	
	130				135					140						
Asp	Asn	Ile	Ile	Phe	Ser	Glu	Glu	Tyr	Asn	Thr	Ser	Asn	Pro	Asp	Leu	
145				150				155						160		
Leu	Leu	Val	Ile	Phe	Gln	Val	Thr	Gly	Ile	Ser	Leu	Leu	Pro	Pro	Leu	
		165					170							175		
Gly	Val	Ala	Ile	Ser	Val	Ile	Ile	Ile	Phe	Tyr	Cys	Tyr	Arg	Val	Asn	
	180						185					190				
Arg	Gln	Gln	Lys	Leu	Ser	Ser	Thr	Trp	Glu	Thr	Gly	Lys	Thr	Arg	Lys	
	195					200					205					
Leu	Met	Glu	Phe	Ser	Glu	His	Cys	Ala	Ile	Ile	Leu	Glu	Asp	Asp	Arg	
	210				215					220						
Ser	Asp	Ile	Ser	Ser	Thr	Cys	Ala	Asn	Asn	Ile	Asn	His	Asn	Thr	Glu	
225				230						235				240		
Leu	Leu	Pro	Ile	Glu	Leu	Asp	Thr	Leu	Val	Gly	Lys	Gly	Arg	Phe	Ala	
		245					250							255		
Glu	Val	Tyr	Lys	Ala	Lys	Leu	Lys	Gln	Asn	Thr	Ser	Glu	Gln	Phe	Glu	
	260					265						270				
Thr	Val	Ala	Val	Lys	Ile	Phe	Pro	Tyr	Glu	Glu	Tyr	Ala	Ser	Trp	Lys	

				85					90					95			
Tyr	Asn	Leu	Met	Arg	Ser	Thr	Ala	Ser	Gly	Leu	Ala	Phe	Leu	His	Asn		
			100					105					110				
Gln	Ile	Gly	Gly	Ser	Lys	Glu	Ser	Asn	Lys	Pro	Ala	Met	Ala	His	Arg		
		115					120				125						
Asp	Ile	Lys	Ser	Lys	Asn	Ile	Met	Tyr	Lys	Asn	Asp	Leu	Thr	Cys	Ala		
		130				135				140							
Ile	Gly	Asp	Leu	Gly	Leu	Ser	Leu	Ser	Lys	Pro	Glu	Asp	Ala	Ala	Ser		
145				150					155						160		
Asp	Ile	Ile	Ala	Asn	Glu	Asn	Tyr	Lys	Cys	Gly	Thr	Val	Arg	Tyr	Leu		
			165					170				175					
Ala	Pro																

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

Thr	Arg	Leu	His	Leu	Cys	His	Cys	Ser	Arg	Glu	Val	Gly	Cys	Asn	Ala		
			5					10					15				
Arg	Thr	Thr	Gly	Trp	Val	Pro	Gly	Ile	Glu	Phe	Leu	Asn	Glu	Thr	Asp		
		20				25					30						
Arg	Ser	Phe	Tyr	Glu	Asn	Thr	Cys	Tyr	Thr	Asp	Gly	Ser	Cys	Tyr	Gln		
	35				40					45							
Ser	Ala	Arg	Pro	Ser	Pro	Glu	Ile	Ser	His	Phe	Gly	Cys	Met	Asp	Glu		
	50				55					60							
Lys	Ser	Val	Thr	Asp	Glu	Thr	Glu	Phe	His	Asp	Thr	Ala	Ala	Lys	Val		
65				70				75						80			
Cys	Thr	Asn	Asn	Thr	Lys	Asp	Pro	His	Ala	Thr	Val	Trp	Ile	Cys	Cys		
			85					90					95				
Asp	Lys	Gly	Asn	Phe	Cys	Ala	Asn	Glu	Thr	Ile	Ile	His	Leu	Ala	Pro		
		100					105						110				
Gly	Pro	Gln	Gln	Ser	Ser	Thr	Trp	Leu	Ile	Leu	Thr	Ile	Leu	Ala	Leu		
		115				120						125					
Leu	Thr																
	130																

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Asp	Leu	Lys	Pro	Glu	Asn												
			5														

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
Asp Leu Ala Ala Arg Asn
5

(2) INFORMATION FOR SEQ ID NO: 37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
Gly Thr Xaa Xaa Tyr Xaa
5

(2) INFORMATION FOR SEQ ID NO: 38:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
Gly Thr Xaa Xaa Phe Xaa
5

(2) INFORMATION FOR SEQ ID NO: 39:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
Gly Ser Xaa Xaa Tyr Xaa
5

(2) INFORMATION FOR SEQ ID NO: 40:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
Gly Ser Xaa Xaa Phe Xaa
5

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
Xaa Pro Ile Lys Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 42:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
Xaa Pro Ile Lys Trp Met
 5

(2) INFORMATION FOR SEQ ID NO: 43:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
Xaa Pro Ile Arg Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 44:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
Xaa Pro Ile Arg Trp Met
 5

(2) INFORMATION FOR SEQ ID NO: 45:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
Xaa Pro Val Lys Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 46:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
Xaa Pro Val Lys Trp Met
 5

(2) INFORMATION FOR SEQ ID NO: 47:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
Xaa Pro Val Arg Trp Thr
 5

(2) INFORMATION FOR SEQ ID NO: 48:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
Xaa Pro Val Arg Trp Met
 5